

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 13, 2005, 08:47:46 ; Search time 219 Seconds
(without alignments)
8054.367 Million cell updates/sec

Title: US-09-721-183-1

Perfect score: 1078
Sequence: 1 ggatatacaagagccaaga.....tgggtctccttgatcggtg 1078

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------|
| 1 | 63.6 | 5.9 | 1141 | 4 | US-09-806-708B-22 |
| 2 | 49.6 | 4.6 | 832 | 4 | US-09-621-976-2813 |
| 3 | 48.4 | 4.5 | 7218 | 1 | US-08-232-463-14 |
| 4 | 43.2 | 4.0 | 601 | 4 | US-09-949-016-156050 |
| 5 | 42.4 | 3.9 | 54161 | 4 | US-09-949-016-11905 |
| 6 | 42 | 3.9 | 78810 | 4 | US-09-949-016-11905 |
| 7 | 42 | 3.9 | 237241 | 4 | US-09-949-016-16101 |
| 8 | 41.6 | 3.9 | 832 | 4 | US-09-621-976-2813 |
| 9 | 40.8 | 3.8 | 151088 | 4 | US-09-949-016-16240 |
| 10 | 40.6 | 3.8 | 487 | 4 | US-09-673-395A-86 |
| 11 | 40.6 | 3.8 | 492 | 4 | US-09-673-395A-110 |
| 12 | 40.6 | 3.8 | 1497 | 4 | US-09-220-132-94 |
| 13 | 40 | 3.7 | 687 | 3 | US-09-134-001C-1857 |
| 14 | 40 | 3.7 | 687 | 3 | US-09-134-001C-2658 |
| 15 | 39.4 | 3.7 | 202111 | 4 | US-09-949-016-13877 |
| 16 | 39.4 | 3.7 | 343352 | 4 | US-09-949-016-13498 |
| 17 | 39.2 | 3.6 | 522 | 4 | US-09-248-796A-7323 |
| 18 | 39.2 | 3.6 | 7218 | 1 | US-08-232-463-14 |
| 19 | 39 | 3.6 | 99500 | 4 | US-09-738-096-10 |
| 20 | 38.6 | 3.6 | 1141 | 4 | US-09-806-708B-22 |
| 21 | 38.4 | 3.6 | 3258 | 4 | US-09-328-352-587 |
| 22 | 38.2 | 3.5 | 246240 | 2 | US-08-724-394A-20 |
| 23 | 38.2 | 3.5 | 246240 | 2 | US-08-724-394A-21 |
| 24 | 38.2 | 3.5 | 246240 | 2 | US-08-724-394A-22 |
| 25 | 38 | 3.5 | 1039 | 4 | US-09-902-540-1280 |
| 26 | 38 | 3.5 | 87470 | 4 | US-09-949-016-15881 |
| 27 | 37.8 | 3.5 | 57178 | 4 | US-09-949-016-12838 |

ALIGNMENTS

RESULT 1

US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342

GENERAL INFORMATION:
; APPLICANT: The University of British Columbia

; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741

; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: US 60/147,133

; PRIOR FILING DATE: 1999-08-04

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 22

; LENGTH: 1141

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; NAME/KEY: promoter

; LOCATION: (1)..(1141)

; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

| | | | | |
|-----------------------|-------|---|-----------------|-------------------|
| Query Match | 5.9% | Score 63.6; | DB 4; | Length 1141; |
| Best Local Similarity | 12.3% | Pred. No. 1.6e-07; | | |
| Matches | 105; | Conservative 297; | Mismatches 450; | Indels 2; Gaps 2; |
| Qy | 53 | AAGGATCCAGGAAATCAACAGTAAAGTGAAGGATGAGCAGCGTCTCTGTTGTTTCAATG | 112 | |
| Db | 270 | AMAYRRWMNNNNNAXAMCKRKYWGNRABVNSTCTTWKSKTKYKTSWANNCRAGD | 329 | |
| Qy | 113 | AGGATAGAGTAAGAGATTGATTTAGATTGCAACAGAGGAATTAGTTAGATACACAGA | 172 | |
| Db | 330 | ANKDHKKWKSAAAGVYNNNNNNNNWYKKARHBBARWVWHSAAKWHANAAYSRKKK | 389 | |
| Qy | 173 | AGAACTTCCTAGCTGAAGATTGTCATAGTGTCTGCTTCTAGATATCTCGGAAAGATT | 232 | |
| Db | 390 | TBYKRRTVMNNNGTTTWKRMWAMYWKMDWBGTNNNNNGRTYYGWTNKKKWTYYK | 449 | |
| Qy | 233 | TGATAATAGTTGTTGTAATAGAGGAGGATATGATGTTTATTGGCCATTTTGGCG | 292 | |
| Db | 450 | WKANNCKRWADHKTCHNNNTTWKMTYNNCWKSKTNGKSHRBAAYVTWYWWRR | 509 | |
| Qy | 293 | GACTCTTCGACTTCTGCTGCTCTCTGAGGATACATTCCAATTCCATCTCGCGAGA | 352 | |
| Db | 510 | YAHANNNNWDYWKACTWYKVCWKNNNYAAWYTKSSWNYTSRYRWKTNNSWRSD | 569 | |
| Qy | 353 | TCCAGTGTCTAGTACTGCTCTCTAGTCCCTTAGTAAACGATCATGTTCAATG | 412 | |

Sequence 17458, A
Sequence 18448, A
Sequence 8976, Ap
Sequence 49764, A
Sequence 49765, A
Sequence 83316, A
Sequence 14143, A
Sequence 12883, A
Sequence 13194, A
Sequence 1, Appli
Sequence 17532, A
Sequence 1, Appli
Sequence 177368,
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16198
; LENGTH: 78810
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(78810)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16198

Query Match 3.9%; Score 42; DB 4; Length 78810;
Best Local Similarity 67.0%; Pred. No. 1.1;
Matches 75; Conservative 0; Mismatches 35; Indels 2; Gaps 1;

Qy 775 ATCACTTTATGATTTGGTATTCCTTAGACTTTTAAATATACTAATGATTTCT--AGT 832
Db 46800 ATCACTGCAATGGAGTTCTCATCTCTTTGACTCTTAAATAGATGAATATTTTTCAT 46859

Qy 833 CTTACTCTAAAGACCTTTGATGTTAAAGAACTCTTCATTTATTTTCATATTC 884
Db 46860 TTATCTTTAAGACATGTGAAGTGTGATCTTGTCTATTTCTTTCATATTC 46911

RESULT 7
US-09-949-016-16101/c
; Sequence 16101, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16101
; LENGTH: 237241
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(237241)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16101

Query Match 3.9%; Score 42; DB 4; Length 237241;
Best Local Similarity 47.4%; Pred. No. 1.8;
Matches 126; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

Qy 678 AGATAATCTCATGCTTATGTTTCCCATCTCGGAATCTTTGTACAGTGGAGTTCCC 737
Db 194379 AGCTAATTATGACCTATATATATCCATTAATAAACCTCAGAAACATGAAGTATTTTAC 194320

Qy 738 CGATGTGTTTTCTTTCTTAGGTGAAGGTTGGCTATATCACTTTATTTGAATTTTGCAAT 797

Db 194319 TGATAATAAATGTTTTATTATTAGGTAAATGATAAACAATGAAACTTAAAGATATAAACAAT 194260
Qy 798 CCTAGACITTTTAAATATACTAATGTATTTCTTACTTCTTAAAGACCTTTTGATCTTA 857
Db 194259 AGGTATTTTCTTCATATCTGCTCTTAAATCTAGGCTTTTCATGTTAGATCCTCTTTAAA 194200
Qy 858 AAGGAATCCTTTTCATTTATTTTCAATATCCCTATCTCATAGGGCCACAAATATTTTAAATACA 917
Db 194199 AAGGTATGTAATAATTAATTTTGTAGTTAGTATATAAATATCACAATATGCTTATAAA 194140
Qy 918 GAGATGATTTTCAAAATATTTTAAACA 943
Db 194139 GTAAAAAATATTGAAATATAAAAAA 194114

RESULT 8
US-09-621-976-2813/c
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENEST.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match 3.9%; Score 41.6; DB 4; Length 832;
Best Local Similarity 10.1%; Pred. No. 0.17;
Matches 38; Conservative 173; Mismatches 167; Indels 0; Gaps 0;

Qy 591 AATGAATGTAAGCTATTTTGGGATCCAGTGTCTATAAACCTTTCTCTTTGTGCACAGA 650
Db 378 AATAATATATTTTGTGYYTWTWTKTWYTYTTRMMWKKARRWYWKSTYACASRY 319
Qy 651 ATCTAACTAGCAAGCCCATTTAGCACCAGATAATTTATCATGTTAGTTTCCCATCTCGG 710
Db 318 RKYTWGWWYMMKRMSTRWYCYMCKWCCMYRGRRCAYTMRGRMWSYAWGKWKMSRSA 259
Qy 711 AAAATCTTTGTACAGTGGGAAGTCCCGATGTGTTTCTTTCTTAGGTGAAGGGTTGG 770
Db 258 MSMTMYKKGSTYWTMKTCTATWCYWKYKRMWSKTCWSGSRGYMTSTSTRSYS 199
Qy 771 CTATATCACTTTTATGAAATTTTCATTTCTTAGACTTTTAAATATACTAATGTTATCTA 830
Db 198 MYWASHMYTMCWWGRRWSTYWTMANGKKWRVATTTWRRAMWWAAATWMMYMWAWCM 139
Qy 831 GTCTTACTTAAAGACCTTTGATGTTTAAAGGAATCCCTTCATTTATTTTCAATTCCTTCATC 890
Db 138 SSRGAAMYRTMMWGYRWKRSYRRTCAWAYAKTKRSYVWCWVKWKRCMMMM 79
Qy 891 TCATAGGGCCACAATTTTATAACAGAGATGTTTCAAAATATTTTAACTACTGTA 950
Db 78 AMAYGKTMKMRACWKTRYRWAWMMWMTTMMMYWYTWYWRAMKRRMMWKRSWSMMW 19
Qy 951 CAGACAGATGCCAGCA 968
Db 18 MAWGTRWAARWWRWYR 1

RESULT 9

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US-09-949-016-16240/c
; Sequence 16240, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16240
; LENGTH: 151088
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(151088)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16240

Query Match          3.8%; Score 40.8; DB 4; Length 151088;
Best Local Similarity 50.5%; Pred. No. 3.1;
Matches 99; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

Qy      801 TAGACTTTTAAATATACATATGTTCTTAGTCTTACTCTTAAGACCTTTTGATGTTAAAG 860
Db      61026 TAGACAATCATATCCACTGCTTTTAAACTGAATTTCTTTAAATAATACATAATAATAA 60967

Qy      861 GAATCCTTCATTATTTTCATATCCCTATCTCATAGGCCACAAATATTTTAAATACAGAG 920
Db      60966 ATAAACTGCATTTCTTAAATCATTAACAAGTGAAGAGGCCACCTTTTCATACATTCCTG 60907

Qy      921 ATGATTTTCAAAATATTTTACAACTGTTACAGACAGATGCCAGCCACTCAGAAAGGAT 980
Db      60906 GTCAATTTTAAACACTATTTTCTACTTTTCCAGTTTGTGGCATGTCTTTTAAATATGTAT 60847

Qy      981 GCCTGCTGTAACAAG 996
Db      60846 GGTACTTTTGGACAG 60831

RESULT 10
US-09-673-395A-86/c
; Sequence 86, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-395A-86

Query Match          3.8%; Score 40.6; DB 4; Length 487;
```

```
Best Local Similarity 73.2%; Pred. No. 0.26;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy      931 AAATATTTTAACTGCTACAGCAGACATGCCAGCCACTCAGAAGGATGCCCTGCTGTA 990
Db      351 AAATGTTTAACTGCTATAGCATAGACTCCCAACCAATCAGATGATGATTTTCAGCCATA 292

Qy      991 AACAAAGCAGTA 1001
Db      291 AACTGCCAGTA 281

RESULT 11
US-09-673-395A-110/c
; Sequence 110, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-395A-110

Query Match          3.8%; Score 40.6; DB 4; Length 492;
Best Local Similarity 73.2%; Pred. No. 0.26;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy      931 AAATATTTTAACTGCTACAGCAGACATGCCAGCCACTCAGAAGGATGCCCTGCTGTA 990
Db      351 AAATGTTTAACTGCTATAGCATAGACTCCCAACCAATCAGATGATGATTTTCAGCCATA 292

Qy      991 AACAAAGCAGTA 1001
Db      291 AACTGCCAGTA 281

RESULT 12
US-09-220-132-94/c
; Sequence 94, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: SHYJIAN, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 1497
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1497)
; OTHER INFORMATION: n = A,T,C or G
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US-09-220-132-94

Query Match 3.8%; Score 40.6; DB 4; Length 1497;
Best Local Similarity 19.2%; Pred. No. 0.43;
Matches 52; Conservative 100; Mismatches 119; Indels 0; Gaps 0;
QY 386 TTAGAGTAACAGCATCATGCTGACGACCAAAATCACCTTCAGCCATGTGGTTCTTC 445
DB 516 WTGGKAWTWAAAWTKRACWAAARKWCMWYTYTYCMCARWTKRCCWATYTW 457
QY 446 ATCATCATGATTTCTTTGGTTGACAAACATCTGCTGCTCAGATGCAAAAAGTACAC 505
DB 456 KSCAWCYTKSYTWRRAWKSCCCCMRGSCYKYMARSCKYGRAMVTKRAAAWTAAWT 397
QY 506 TGGGAATGACGTGAAGTGGTGAATTTAGTTTGGTATTATTTAAACTACATTTTA 565
DB 396 KKKKTWNAERWKKKSYGGRWKSYYTYTYCMRKTYCMWTTTKRAAAAMCMWGRWTTX 337
QY 566 GTTTTCTCTCTCTCTATGTTGCAATGAATGTAAAGTATTGGGATCCAGTGCTTATA 625
DB 336 RWNKKYKMSYCYCCYTYWKSCKGAAAAAARAKWRKTYKSMWAWKKGKKTW 277
QY 626 AACCTTTCCTCTCTTGTGTCACAGAAATGTAA 656
DB 276 MWAYKMKTYWRRRTCKKACAGAGTAAGTAA 246

RESULT 13

US-09-134-001C-1857/c
; Sequence 1857, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1857
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1857

Query Match 3.7%; Score 40; DB 3; Length 687;
Best Local Similarity 47.9%; Pred. No. 0.44; Indels 125; Gaps 0;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
QY 702 CCATCTCGGAAATCTTTGTACAGTGGGAAGTTCCCGAGTGTGTTTTCTTCTTAGGTG 761
DB 655 CCAAAATGGATTTTACTTCTCCATAAGAAAAATCATCAATATTTTTCATCTTTAAGAA 596
QY 762 AAGGGTGGCTATATCATCTTTATTTGAATTTTGGATTCCTTAGACTTTTAAATAATATA 821
DB 595 GTAATTTCTATTTTCAATCTCAACATTTGTACCTTCTGAAATATCTTTTAAATAT 536
QY 822 TGTATTTCTACTTCTTAAAGACCTTTGATGTTAAAGAACTCTTCATTTATTTTCATA 881
DB 535 TTGATTTTGTAAACCAATTAATACATTTTCTATTTCCAAAGAAATCAAAATCTTCTCT 476
QY 882 TTCCCTATCTCATAGGCGCCACAATTTATTTAAATACAGAGATGATTTTCAAAATATTTAA 941
DB 475 TTAATTTTCTATATAATCTGATTTAATAAATATTTAGACCAAAATATATGAAATTAATA 416

RESULT 14

US-09-134-001C-2658/c
; Sequence 2658, Application US/09134001C

Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2658
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2658

Query Match 3.7%; Score 40; DB 3; Length 687;
Best Local Similarity 47.9%; Pred. No. 0.44; Indels 125; Gaps 0;
Matches 115; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
QY 702 CCATCTCGGAAATCTTTGTACAGTGGGAAGTTCCCGAGTGTGTTTTCTTCTTAGGTG 761
DB 655 CCAAAATGGATTTTACTTCTCCATAAGAAAAATCATCAATATTTTTCATCTTTAAGAA 596
QY 762 AAGGGTGGCTATATCATCTTTATTTGAATTTTGGATTCCTTAGACTTTTAAATAATATA 821
DB 595 GTAATTTCTATTTTCAATCTCAACATTTGTACCTTCTGAAATATCTTTTAAATAT 536
QY 822 TGTATTTCTACTTCTTAAAGACCTTTGATGTTAAAGAACTCTTCATTTATTTTCATA 881
DB 535 TTGATTTTGTAAACCAATTAATACATTTTCTATTTCCAAAGAAATCAAAATCTTCTCT 476
QY 882 TTCCCTATCTCATAGGCGCCACAATTTATTTAAATACAGAGATGATTTTCAAAATATTTAA 941
DB 475 TTAATTTTCTATATAATCTGATTTAATAAATATTTAGACCAAAATATATGAAATTAATA 416

RESULT 15

US-09-949-016-13877/c
; Sequence 13877, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13877
; LENGTH: 202111
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(202111)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13877

Query Match 3.7%; Score 39.4; DB 4; Length 202111;
Best Local Similarity 55.5%; Pred. No. 8.7; Indels 1; Gaps 1;
Matches 96; Conservative 0; Mismatches 76; Indels 1; Gaps 1;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 13, 2005, 13:40:12 ; Search time 764 Seconds
(without alignments)
8858.687 Million cell updates/sec

Title: US-09-721-183-1
Perfect score: 1078
Sequence: 1 ggaatgatacaagagccaaga.....tggtgttccttgaatcg 1078

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6330947 seqs, 3139163630 residues

Total number of hits satisfying chosen parameters: 12661894

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|---------------------------------------|
| 1 | 1063.8 | 98.7 | 2510 | 17 | US-10-104-047-1599 Sequence 1599, Ap |
| 2 | 1055 | 97.9 | 1879 | 17 | US-10-104-047-1376 Sequence 1376, Ap |
| 3 | 117.6 | 10.9 | 44546 | 13 | US-10-087-192-625 Sequence 625, App |
| C 4 | 61 | 5.7 | 262 | 11 | US-09-864-408A-5207 Sequence 5207, Ap |
| 5 | 50.4 | 4.7 | 176 | 9 | US-09-867-701-9147 Sequence 9147, Ap |
| 6 | 49.4 | 4.6 | 201 | 19 | US-10-741-601-22105 Sequence 22105, A |
| 7 | 49.4 | 4.6 | 201 | 19 | US-10-741-601-22106 Sequence 22106, A |

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| 8 | 49.4 | 4.6 | 201 | 19 | US-10-741-601-22107 Sequence 22107, A |
| 9 | 49.4 | 4.6 | 201 | 21 | US-10-741-600-62317 Sequence 62317, A |
| 10 | 49.4 | 4.6 | 201 | 21 | US-10-741-600-62318 Sequence 62318, A |
| 11 | 49.4 | 4.6 | 201 | 21 | US-10-741-600-62319 Sequence 62319, A |
| 12 | 49.4 | 4.6 | 398287 | 19 | US-10-741-601-5719 Sequence 5719, Ap |
| 13 | 49.4 | 4.6 | 398287 | 21 | US-10-741-601-5719 Sequence 5719, Ap |
| 14 | 49 | 4.5 | 6077 | 15 | US-10-311-455-2192 Sequence 2192, Ap |
| 15 | 48 | 4.5 | 553 | 13 | US-10-027-632-259014 Sequence 259014, A |
| 16 | 48 | 4.5 | 553 | 13 | US-10-027-632-259015 Sequence 259015, A |
| 17 | 48 | 4.5 | 553 | 17 | US-10-027-632-259014 Sequence 259014, A |
| 18 | 48 | 4.5 | 553 | 17 | US-10-027-632-259015 Sequence 259015, A |
| 19 | 46 | 4.3 | 5930 | 15 | US-10-311-455-490 Sequence 490, App |
| 20 | 45.8 | 4.2 | 16811 | 15 | US-10-311-455-1919 Sequence 1919, Ap |
| C 21 | 45.6 | 4.2 | 16569 | 22 | US-10-488-618-1 Sequence 1, Appli |
| 22 | 44.6 | 4.1 | 5520 | 15 | US-10-311-455-1492 Sequence 1492, Ap |
| 23 | 44.2 | 4.1 | 14615 | 18 | US-10-221-714A-430 Sequence 430, App |
| C 24 | 44 | 4.1 | 7040 | 15 | US-10-172-086-13 Sequence 13, Appl |
| C 25 | 44 | 4.1 | 7040 | 18 | US-10-221-714A-161 Sequence 161, App |
| C 26 | 44 | 4.1 | 7040 | 19 | US-10-311-507-47 Sequence 47, Appl |
| C 27 | 44 | 4.1 | 7040 | 20 | US-10-480-846-13 Sequence 13, Appl |
| C 28 | 44 | 4.1 | 7040 | 20 | US-10-473-126-173 Sequence 173, App |
| C 29 | 44 | 4.1 | 7040 | 20 | US-10-473-126-319 Sequence 319, App |
| 30 | 43.8 | 4.1 | 6076 | 18 | US-10-221-714A-385 Sequence 385, App |
| 31 | 43.8 | 4.1 | 6189 | 15 | US-10-240-485-145 Sequence 145, App |
| 32 | 43.8 | 4.1 | 6189 | 18 | US-10-221-714A-321 Sequence 321, App |
| 33 | 43.6 | 4.0 | 6075 | 15 | US-10-311-455-1523 Sequence 1523, Ap |
| 34 | 43.4 | 4.0 | 15674 | 15 | US-10-311-455-336 Sequence 336, App |
| 35 | 43.4 | 4.0 | 15674 | 15 | US-10-240-485-30 Sequence 30, Appl |
| 36 | 43.2 | 4.0 | 11092 | 15 | US-10-311-455-1485 Sequence 1485, Ap |
| 37 | 43 | 4.0 | 721 | 20 | US-10-363-345A-3373 Sequence 3373, Ap |
| C 38 | 43 | 4.0 | 721 | 20 | US-10-363-345A-3374 Sequence 3374, Ap |
| 39 | 43 | 4.0 | 721 | 21 | US-10-363-483A-3373 Sequence 3373, Ap |
| C 40 | 43 | 4.0 | 721 | 21 | US-10-363-483A-3374 Sequence 3374, Ap |
| C 41 | 42.8 | 4.0 | 663 | 13 | US-10-027-632-236652 Sequence 236652, A |
| C 42 | 42.8 | 4.0 | 663 | 17 | US-10-027-632-236652 Sequence 236652, A |
| 43 | 42.8 | 4.0 | 12138 | 15 | US-10-311-455-1602 Sequence 1602, Ap |
| 44 | 42.8 | 4.0 | 12138 | 15 | US-10-311-455-1602 Sequence 1602, Ap |
| 45 | 42.8 | 4.0 | 3673778 | 16 | US-10-312-841-2 Sequence 2, Appli |

ALIGNMENTS

RESULT 1
US-10-104-047-1599
; Sequence 1599, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1599
; LENGTH: 2510
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1599

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| Query Match | 98.7% | Score 1063.8; | DB 17; | Length 2510; |
| Best Local Similarity | 99.7% | Pred. No. 1.9e-259; | | |
| Matches 1076; | Conservative | 0; | Mismatches | 2; |
| | | | Indels | 1; |
| | | | Gaps | 1; |
| Qy | 1 | GGATGATACAGAGCCAGGACATTTGAGTTGTCGTTAGTAGAGGATC | 60 | |
| Db | 1432 | GGATGATACAGAGCCAGGACATTTGAGTTGTCGTTAGTAGAGGATC | 1491 | |
| Qy | 61 | CAGGAAATCAACAGTAGTAGAGGATCAGGATCTCTTGGTTTTCATTGAGGATAGA | 120 | |

Db 1492 CAGGGAATCAACAGTAAGTGGAGTACAGAGTGTCTCTTGGTTTTTCATTGAGGATAGA 1551
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Qy 181 CTAGCCTTGAAGATTGTCTAGTGTCTGTCTTCTAGATATCTGGGAAAGATTTTGATAATA 240
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Qy 421 TCACCTTCAGCCATGTGGTTTCTTCATCATCATGAGATTTCTTTGGTTGACAAACATCT 480
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RESULT 2
US-10-104-047-1376
; Sequence 1376, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1376
; LENGTH: 1879
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-104-047-1376

Query Match 97.9%; Score 1055; DB 17; Length 1879;
Best Local Similarity 99.8%; Pred. No. 2.8e-257;
Matches 1077; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy 61 CAGGGAATCAACAGTAACTGAGGATGACGCGTCTCTTGGCTTTTCATTGAGGATAGA 120
Db 862 CAGGGAATCAACAGTAACTGAGGATGACGCGTCTCTTGGCTTTTCATTGAGGATAGA 921
Qy 121 GTAAGAGATTGAGTTTGTAGATTGCAACAGAGGAAATAGTTTGTAGATACACAGGAAGACTTC 180
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